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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=25; hr=18; min=3; sec=53; ms=549; ]

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Reviewer Comments:

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.  
Nadler, Lee M.  
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH  
INCREASED IMMUNOGENICITY AND USES THEREFOR

The above (ii) TITLE OF INVENTION: line exceeds the Sequence Rules' required 72-character limit (this includes white spaces). Please insert a hard return after "WITH" above.

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 329 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Per the Sequence Rules, the "INFORMATION FOR SEQ ID NO:" heading is always preceded by a "(2)," regardless of the Sequence ID number.

Please do not number this heading consecutively. Replace the above (3) INFORMATION FOR SEQ ID NO:2: with (2) INFORMATION FOR SEQ ID NO:2:. Please do the same with the subsequent sequences.

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTTAGAGCACA

Please replace the (10) INFORMATION FOR SEQ ID NO:9: with (2) INFORMATION FOR SEQ ID NO:9:. Please insert a space after each group of 10 nucleotides, and insert the cumulative nucleotide total at the right margin. These errors occur in subsequent sequences, too.

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Application No: 10767561 Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-17 17:06:18.746  
 Finished: 2008-01-17 17:06:19.572  
 Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 826 ms  
 Total Warnings: 0  
 Total Errors: 66  
 No. of SeqIDs Defined: 17  
 Actual SeqID Count: 1

Error code	Error Description
E 200	Mandatory field label missing: in 2_i_C
E 200	Mandatory field label missing: in 2_ii
E 200	Mandatory field label missing: in 2_vi_D
E 200	Mandatory field label missing: in 2_i_C
E 104	Command to process tag does not exist: Tag: 11
E 104	Command to process tag does not exist: Tag: 11_i
E 104	Command to process tag does not exist: Tag: 11_i_A
E 104	Command to process tag does not exist: Tag: 11_i_B
E 104	Command to process tag does not exist: Tag: 11_i_C
E 104	Command to process tag does not exist: Tag: 11_i_D
E 104	Command to process tag does not exist: Tag: 11_ii
E 104	Command to process tag does not exist: Tag: 11_xi
E 104	Command to process tag does not exist: Tag: 12
E 104	Command to process tag does not exist: Tag: 12_i
E 104	Command to process tag does not exist: Tag: 12_i_A
E 104	Command to process tag does not exist: Tag: 12_i_B
E 104	Command to process tag does not exist: Tag: 12_i_C
E 104	Command to process tag does not exist: Tag: 12_i_D
E 104	Command to process tag does not exist: Tag: 12_ii
E 104	Command to process tag does not exist: Tag: 12_xi

**Input Set:**

**Output Set:**

**Started:** 2008-01-17 17:06:18.746  
**Finished:** 2008-01-17 17:06:19.572  
**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 826 ms  
**Total Warnings:** 0  
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Error code	Error Description
E 104	Command to process tag does not exist: Tag: 12_i
E 104	Command to process tag does not exist: Tag: 12_i_A
E 104	Command to process tag does not exist: Tag: 12_i_B
E 104	Command to process tag does not exist: Tag: 12_i_C This error has occurred more than 20 times, will not be displayed
E 252	Calc# of Seq. differs from actual; 17 seqIds defined; count=1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.  
Nadler, Lee M.  
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH INCREASED IMMUNOGENICITY  
AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley Hoag  
(B) STREET: 155 Seaport Boulevard  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10767561  
(B) FILING DATE: 2004-01-28

(vii) PRIOR APPLICATION DATA:

(B) FILING DATE: 28-JAN-2004  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/101,624;  
(B) FILING DATE: 26-JUL-1993;  
(A) APPLICATION NUMBER: 08/109,393;  
(b) FILING DATE: 19-AUG-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Russell, Hathaway P.  
(B) REGISTRATION NUMBER: 46,488  
(C) REFERENCE/DOCKET NUMBER: WYS-018.04

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000  
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
Met Asp Pro	
1	
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
5 10 15	
CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
20 25 30 35	
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
40 45 50	
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
55 60 65	
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
70 75 80	
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
85 90 95	
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
100 105 110 115	
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
120 125 130	

GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
135 140 145	
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
150 155 160	
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
165 170 175	
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
180 185 190 195	
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	
200 205 210	
AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT	787
Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	
215 220 225	
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA	835
Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	
230 235 240	
GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT	883
Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	
245 250 255	
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG	931
Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	
260 265 270 275	
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG	979
Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	
280 285 290	
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT	1027
Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	
295 300 305	
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC	1075
Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	
310 315 320	
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA	1120
Lys Ser Asp Thr Cys Phe	
325	

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
 1             5             10             15

Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
      20             25             30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
      35             40             45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
 50             55             60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
 65             70             75             80

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
      85             90             95

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
      100            105            110

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
      115            120            125

Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
      130            135            140

Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
      145            150            155            160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
      165            170            175

Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
      180            185            190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
      195            200            205

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
      210            215            220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
      225            230            235            240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
      245            250            255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
```



260

265

270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu  
 275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro  
 290 295 300

Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser  
 305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe  
 325

## (4) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..1028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60

CCTGTAGACG TGTTCAGAA CTTACGGAAG CACCCACG ATG GAC 104  
 Met Asp  
 1

CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG 152  
 Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu  
 5 10 15

CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG 200  
 Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly  
 20 25 30

ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG 248  
 Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu  
 35 40 45 50

AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC 296  
 Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr  
 55 60 65

GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC 342  
 Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr  
 70 75 80

CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC	382
Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His	
85 90 95	
AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA	440
Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys	
100 105 110	
AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG	488
Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu	
115 120 125 130	
TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT	536
Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn	
135 140 145	
GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT	584
Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly	
150 155 160	
CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT	632
His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn	
165 170 175	
GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG	680
Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu	
180 185 190	
TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG	728
Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp	
195 200 205 210	
CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC	776
His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser	
215 220 225	
TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT	814
Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr	
230 235 240	
TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG	872
Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met	
245 250 255	
CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC	920
Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro	
260 265 270	
AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG	968
Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu	
275 280 285 290	
ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA	1016
Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro	
295 300 305	

AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT 1065  
 Asn Ala Glu

TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA 1115

ATTCTACAGT TGAATAATTA AAGAAC 1151

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Pro	Arg	Cys	Thr	Met	Gly	Leu	Ala	Ile	Leu	Ile	Phe	Val	Thr	1	5	10	15
Val	Leu	Leu	Ile	Ser	Asp	Ala	Val	Ser	Val	Glu	Thr	Gln	Ala	Tyr	Phe	20	25	30	
Asn	Gly	Thr	Ala	Tyr	Leu	Pro	Cys	Pro	Phe	Thr	Lys	Ala	Gln	Asn	Ile	35	40	45	
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Gln	Lys	Leu	Val	50	55	60	
Leu	Tyr	Glu	His	Tyr	Leu	Gly	Thr	Glu	Lys	Leu	Asp	Ser	Val	Asn	Ala	65	70	75	80
Lys	Tyr	Leu	Gly	Arg	Thr	Ser	Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg	85	90	95	
Leu	His	Asn	Val	Gln	Ile	Lys	Asp	Met	Gly	Ser	Tyr	Asp	Cys	Phe	Ile	100	105	110	
Gln	Lys	Lys	Pro	Pro	Thr	Gly	Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr	115	120	125	
Glu	Leu	Ser	Val	Ile	Ala	Asn	Phe	Ser	Glu	Pro	Glu	Ile	Lys	Leu	Ala	130	135	140	
Gln	Asn	Val	Thr	Gly	Asn	Ser	Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys	145	150	155	160
Gln	Gly	His	Pro	Lys	Pro	Lys	Lys	Met	Tyr	Phe	Leu	Ile	Thr	Asn	Ser	165	170	175	
Thr	Asn	Glu	Tyr	Gly	Asp	Asn	Met	Gln	Ile	Ser	Gln	Asp	Asn	Val	Thr	180	185	190	

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly  
 195 200 205  
 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys  
 210 215 220  
 Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln  
 225 230 235 240  
 Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu  
 245 250 255  
 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser  
 260 265 270  
 Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp  
 275 280 285  
 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala  
 290 295 300  
 Lys Pro Asn Ala Glu  
 305

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGAAAA AGTGATTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60  
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120  
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180  
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240  
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC 300

CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser

-30

-25

AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401

Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu

-20

-15

-10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449

Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu

-5

1

5

10

GTG GCA AC